

## **SEQUENCE LISTING**

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Adams, Camilia W.  
Ashkenazi, Avi J.  
Chuntharapai, Anan  
Kim, Kyung J.

10 (ii) TITLE OF INVENTION: Apo-2 Receptor

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

15                   (A) ADDRESSEE: Genentech, Inc.  
                     (B) STREET: 1 DNA Way  
                     (C) CITY: South San Francisco  
                     (D) STATE: California  
                     (E) COUNTRY: USA  
20                   (F) ZIP: 94080

25 (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

30 (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Marschang, Diane L.  
(B) REGISTRATION NUMBER: 35,600  
(C) REFERENCE/DOCKET NUMBER: P1101R2

(ix) TELECOMMUNICATION INFORMATION:  
40 (A) TELEPHONE: 650/225-5416  
      (B) TELEFAX: 650/952-9881  
(2) INFORMATION FOR SEO ID NO:1:

(2) INFORMATION FOR SEQ ID NO:1:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 411 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

50 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg  
1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro  
20 25 30

Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val  
35 40 45

60 Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp  
50 55 60

Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser  
65 70 75

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Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Glu Asp  
80 85 90

Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr  
5 95 100 105

His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp  
110 115 120

10 Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr  
125 130 135

Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro  
140 145 150

15 Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val  
155 160 165

Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His  
20 170 175 180

Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val  
185 190 195

25 Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys  
200 205 210

Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Asp  
215 220 225

30 Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp  
230 235 240

Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val  
35 245 250 255

Pro-Glu-Gln-Glu-Met-Glu-Val-Gln-Glu-Pro-Ala-Glu-Pro-Thr-Gly  
260 265 270

40 Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro  
275 280 285

Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala  
290 295 300

45 Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp  
305 310 315

Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg  
50 320 325 330

Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu  
335 340 345

55 Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp  
350 355 360

Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp  
60 365 370 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu  
380 385 390

Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn

Ala Asp Ser Ala Xaa Ser  
410 411

5

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

15

CCACACGCGTC CGCATAAAATC AGCACACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100

20

CCACACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145  
Met Glu  
1

25

CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184  
Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg  
5 10 15

30

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223  
Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala  
20 25

35

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262  
Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val  
30 35 40

GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301  
Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala  
45 50

40

CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340  
Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala  
55 60 65

45

GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379  
Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu  
70 75 80

50

TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418  
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp  
85 90

55

TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457  
Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His  
95 100 105

TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT 496  
Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys  
110 115

60

GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC 535  
Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr  
120 125 130

574

	AGA AAC ACA GTC GT CAG TGC GAA GAA GGC ACC TTC	135	140	145
	Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg			
5	GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA	150	155	613
	Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr			
10	GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA	160	165	652
	Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr			
	160 165 170			
15	CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC	175	180	691
	Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly			
	175 180			
20	ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT	185	190	730
	Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile			
	185 190 195			
25	GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA	200	205	769
	Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys			
	200 205 210			
30	GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT GGT GGT	215	220	808
	Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly			
	215 220			
35	GGG GAC CCT GAG CGT GTG GAC AGA AGC TCA CAA CGA CCT	225	230	847
	Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro			
	225 230 235			
40	GGG GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC	240	245	886
	Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile			
	240 245			
	TTG-CAG-CCC-ACC-CAG-GTC-CCT-GAG-CAG-GAA-ATG-GAA-GTC	250	255	925
	Leu Gln Pro Thr Gln Val Pro Glu Gln Glu Met Glu Val			
	250 255 260			
45	CAG GAG CCA GCA GAG CCA ACA GGT GTC AAC ATG TTG TCC	265	270	964
	Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser			
	265 270 275			
50	CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG GCA GAA GCT	280	285	1003
	Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala			
	280 285			
55	GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT	290	295	1042
	Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn			
	290 295 300			
	GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT	305	310	1081
	Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp			
	305 310			
60	GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG	315	320	1120
	Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro			
	315 320 325			
	CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG	330	335	1159
	Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys			
	330 335 340			

1000527981-240204

GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC 1198  
 Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu  
 345 350

5 TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237  
 Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg  
 355 360 365

GAT GCC TCT GTC TAC ACC CTG CTG GAT GCC TTG GAG ACG 1276  
 10 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr  
 370 375

CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315  
 Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His  
 15 380 385 390

TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354  
 Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn  
 20 395 400 405

GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400  
 Ala Asp Ser Ala Xaa Ser  
 410 411

25 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450  
 AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACCTT TTCACTGCAC 1550  
 30 TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

GTCTGGATCA TTCCGTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA 1650.

35 TTGTTTCAC AGCACTTTT TATCCTAACG TAAATGCTTT ATTTATTTAT 1700  
 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAG 1750

GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTGGCC GCCATGGCC 1799

40 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
 45 (A) LENGTH: 70 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

55 GCTAAAGCTG AGGCAGCGGG 70

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
 60 (A) LENGTH: 29 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

5 (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: Nucleic Acid  
 10 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

20 (2) INFORMATION FOR SEQ ID NO:6:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 930 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

30 ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36  
 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe  
 1 5 10

35 TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75  
 Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile  
 15 20 25

40 CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114  
 Pro-Leu-Val-Val-Pro-Phe-Tyr-Ala-Ala-Gln-Pro-Ala-Met  
 30 35

45 GCC GAG GTG CAG CTG GTG CAG TCT GGG GGA GGT GTG GAA 153  
 Ala Glu Val Gln Leu Val Gln Ser Gly Gly Val Glu  
 40 45 50

50 CGG CCG GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT 192  
 Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser  
 55 60

55 GGA TTC ACC TTT GAT GAT TAT GGC ATG AGC TGG GTC CGC 231  
 Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg  
 65 70 75

60 CAA GCT CCA GGG AAG GGG CTG GAG TGG GTC TCT GGT ATT 270  
 Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile  
 80 85 90

65 AAT TGG AAT GGT GGT AGC ACA GGA TAT GCA GAC TCT GTG 309  
 Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val  
 95 100

70 AAG GGC CGA GTC ACC ATC TCC AGA GAC AAC GCC AAG AAC 348  
 Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn  
 105 110 115

387

TCC CTG TAT CT	A ATG AAC AGC	CTG AGA GCC GAG	
Ser Leu Tyr	Leu Gln Met Asn Ser	Leu Arg Ala Glu Asp	
120		125	
<b>5</b>	ACG GCC GTA TAT TAC TGT GCG AAA ATC CTG GGT GCC GGA	426	
	Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala Gly		
	130	135	140
<b>10</b>	CGG GGC TGG TAC TTC GAT CTC TGG GGG AAG GGG ACC ACG	465	
	Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr		
	145	150	155
<b>15</b>	GTC ACC GTC TCG AGT GGT GGA GGC GGT TCA GGC GGA GGT	504	
	Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly		
	160	165	
<b>20</b>	GGC AGC GGC GGT GGC GGA TCG TCT GAG CTG ACT CAG GAC	543	
	Gly Ser Gly Gly Ser Ser Glu Leu Thr Gln Asp		
	170	175	180
<b>25</b>	CCT GCT GTG TCT GTG GCC TTG GGA CAG ACA GTC AGG ATC	582	
	Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile		
	185	190	
<b>30</b>	ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT TAT GCA AGC	621	
	Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser		
	195	200	205
<b>35</b>	TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC	660	
	Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val		
	210	215	220
<b>40</b>	ATC TAT GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC	699	
	Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp		
	225	230	
<b>45</b>	CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA GCT TCC TTG	738	
	Arg Phe Ser Gly Ser Ser Gly Asn Thr Ala Ser Leu		
	235	240	245
<b>50</b>	ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG GCT GAC TAT	777	
	Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr		
	250	255	
<b>55</b>	TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC CAT GTG GTA	816	
	Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val		
	260	265	270
<b>60</b>	TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT GCG GCC	855	
	Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala		
	275	280	285
<b>65</b>	GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA GAA CAA AAA	894	
	Ala His His His His His Gly Ala Ala Glu Gln Lys		
	290	295	
<b>70</b>	CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA TAG	930	
	Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala		
	300	305	309

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 939 base pairs

- (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

40052798-420204

	ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
10	Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
	1 5 10
	TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
	Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
15	15 20 25
	CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
	Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met
	30 35
20	GCC GGG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTC 153
	Ala Gly Val Gln Leu Val Glu Ser Gly Gly Leu Val
	40 45 50
25	CAG CCT GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT 192
	Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
	55 60
30	GGA TTC ACC TTT AGT AGC TAT TGG ATG AGC TGG GTC CGC 231
	Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg
	65 70 75
	CAG GCT CCA GGG AAG GGG CTG GAG TGG GTG GCC AAC ATA 270
	Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile
35	80 85 90
	AAG CAA GAT GGA AGT GAG AAA TAC TAT GTG GAC TCT GTG 309
	Lys Gln Asp Gly Ser Glu Lys Tyr Val Asp Ser Val
	95 100
40	AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC 348
	Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
	105 110 115
45	TCA CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC 387
	Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
	120 125
50	ACG GCT GTG TAT TAC TGT GCG AGA GAT CTT TTA AAG GTC 426
	Thr Ala Val Tyr Tyr Cys Ala Arg Asp Leu Leu Lys Val
	130 135 140
	AAG GGC AGC TCG TCT GGG TGG TTC GAC CCC TGG GGG AGA 465
	Lys Gly Ser Ser Ser Gly Trp Phe Asp Pro Trp Gly Arg
55	145 150 155
	145 150 155
	GGG ACC ACG GTC ACC GTC TCG AGT GGT GGA GGC GGT TCA 504
	Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser
	160 165
60	GGC GGA GGT GGT AGC GGC GGT GGC GGA TCG TCT GAG CTG 543
	Gly Gly Gly Ser Gly Gly Gly Ser Ser Glu Leu
	170 175 180
	ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG ACA 582

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Thr Gln Asp Pro ~~Ile~~ Val Ser Val Ala Leu Gly Gln  
185 190

5 GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT 621  
Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr  
195 200 205

10 TAT GCA AGC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT 660  
Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro  
210 215 220

GTA CTT GTC ATC TAT GGT AAA AAC AAC CGG CCC TCA GGG 699  
Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly  
225 230

15 ATC CCA GAC CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA 738  
Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Asn Thr  
235 240 245

20 GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG 777  
Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu  
250 255

25 GCT GAC TAT TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC 816  
Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn  
260 265 270

30 CAT GTG GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA 855  
His Val Val Phe Gly Gly Thr Lys Leu Thr Val Leu  
275 280 285

GGT GCG GCC GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA 894  
Gly Ala Ala Ala His His His His His Gly Ala Ala  
290 295

35 GAA CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC 933  
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala  
300 305 310

40 GCA TAG 939  
Ala  
312

(2) INFORMATION FOR SEQ ID NO:8:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 933 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
50 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

55 ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36  
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe  
1 5 10

60 TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75  
Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile  
15 20 25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114  
Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met

GCC CAG GTG CAG CTG GTG CAG TCT GGG GGA GGC GTG GTC 153  
 Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val  
 5 40 45 50

CAG CCT GGG CGG TCC CTG AGA CTC TCC TGT GCA GCT TCT 192  
 Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser  
 10 55~ 60

GGG TTC ATT TTC AGT AGT TAT GGG ATG CAC TGG GTC CGC 231  
 Gly Phe Ile Phe Ser Ser Tyr Gly Met His Trp Val Arg  
 65 70 75

15 CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG GCA GGT ATT 270  
 Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile  
 80 85 90

TTT TAT GAT GGA GGT AAT AAA TAC TAT GCA GAC TCC GTG 309  
 Phe Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val  
 20 95 100

AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC 348  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn  
 25 105 110 115

ACG CTG TAT CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC 387  
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp  
 30 120 125

ACG GCT GTG TAT TAC TGT GCG AGA GAT AGG GGC TAC TAC 426  
 Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Tyr Tyr  
 35 130 135 140

TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC 465  
 Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val  
 145 150 155

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TCC TCA GGT GGA GGC GGT TCA GGC GGA GGT GGC TCT GGC 504  
 Ser Ser Gly Gly Ser Gly Gly Gly Ser Gly  
 40 160 165

GGT GGC GGA TCG CAG TCT GTG TTG ACG CAG CCG CCC TCA 543  
 Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser  
 45 170 175 180

GTG TCT GGG GCC CCA GGA CAG AGG GTC ACC ATC TCC TGC 582  
 Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys  
 50 185 190

ACT GGG AGA AGC TCC AAC ATC GGG GCA GGT CAT GAT GTA 621  
 Thr Gly Arg Ser Ser Asn Ile Gly Ala Gly His Asp Val  
 195 200 205

CAC TGG TAC CAG CAA CTT CCA GGA ACA GCC CCC AAA CTC 660  
 His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu  
 55 210 215 220

CTC ATC TAT GAT GAC AGC AAT CGG CCC TCA GGG GTC CCT 699  
 Leu Ile Tyr Asp Asp Ser Asn Arg Pro Ser Gly Val Pro  
 60 225 230

GAC CGA TTC TCT GGC TCC AGG TCT GGC ACC TCA GCC TCC 738  
 Asp Arg Phe Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser

235

240

245

CTG GCC ATC ACT GGG CTC CAG GCT GAA GAT GAG GCT GAT 777  
 Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp  
 5 250 255

TAT TAC TGC CAG TCC TAT GAC AGC AGC CTG AGG GGT TCG 816  
 Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Arg Gly Ser  
 10 260 265 270

GTA TTC GGC GGA GGG ACC AAG GTC ACT GTC CTA GGT GCG 855  
 Val Phe Gly Gly Thr Lys Val Thr Val Leu Gly Ala  
 15 275 280 285

GCC GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA GAA CAA 894  
 Ala Ala His His His His His Gly Ala Ala Glu Gln  
 290 295

AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA 930  
 20 Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
 300 305 310

TAG 933

## 25 (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile  
 35 1 5 10 15

Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro  
 20 25 30

40 Phe Tyr Ala Ala Gln Pro Ala Met Ala Glu Val Gln Leu Val Gln  
 35 40 45

Ser Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser  
 50 55 60

45 Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp  
 65 70 75

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile  
 50 80 85 90

Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly  
 95 100 105

55 Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 110 115 120

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 125 130 135

60 Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp  
 140 145 150

Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser

55

160

165

Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser Glu Leu Thr Gln  
 170 175 180

5

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr  
 185 190 195

10

Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln  
 200 205 210

Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn  
 215 220 225

15

Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser  
 230 235 240

Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp  
 245 250 255

20

Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His  
 260 265 270

25

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala  
 275 280 285

Ala His His His His His Gly Ala Ala Glu Gln Lys Leu Ile  
 290 295 300

30

Ser Glu Glu Asp Leu Asn Gly Ala Ala  
 305 309

(2) INFORMATION FOR SEQ ID NO:10:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile  
 1 5 10 15

45

Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro  
 20 25 30

Phe Tyr Ala Ala Gln Pro Ala Met Ala Gly Val Gln Leu Val Glu  
 35 40 45

50

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser  
 50 55 60

55

Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp  
 65 70 75

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile  
 80 85 90

60

Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys Gly  
 95 100 105

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 110 115 120

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 125 130 135

5 Ala Arg Asp Leu Leu Lys Val Lys Gly Ser Ser Ser Gly Trp Phe  
 140 145 150

Asp Pro Trp Gly Arg Gly Thr Thr Val Thr Val Ser Ser Gly Gly  
 155 160 165

10 Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Ser Glu  
 170 175 180

Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val  
 185 190 195

Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser  
 200 205 210

20 Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr  
 215 220 225

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly  
 230 235 240

25 Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln  
 245 250 255

Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser  
 260 265 270

Gly Asn His Val Val Phe Gly Gly Thr Lys Leu Thr Val Leu  
 275 280 285

30 35 Gly Ala Ala Ala His His His His His Gly Ala Ala Glu Gln  
 290 295 300

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Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
 305 310 312

40

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

50

Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile  
 1 5 10 15

Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro  
 20 25 30

55

Phe Tyr Ala Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln  
 35 40 45

60

Ser Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser  
 50 55 60

Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr Gly Met His Trp  
 65 70 75

P1101R2

Val Arg Gln Al [REDACTED] Gly Lys Gly Leu Glu Trp Val [REDACTED] Gly Ile  
80 85 90

5 Phe Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly  
95 100 105

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu  
110 115 120

10 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
125 130 135

Ala Arg Asp Arg Gly Tyr Tyr Met Asp Val Trp Gly Lys Gly  
140 145 150

15 Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly  
155 160 165

Gly Ser Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro  
20 170 175 180

Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr  
185 190 195

25 Gly Arg Ser Ser Asn Ile Gly Ala Gly His Asp Val His Trp Tyr  
200 205 210

Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asp  
215 220 225

30 Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Arg  
230 235 240

Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu  
35 245 250 255

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Arg  
260 265 270

40 Gly Ser Val Phe Gly Gly Thr Lys Val Thr Val Leu Gly Ala  
275 280 285

Ala Ala His His His His His Gly Ala Ala Glu Gln Lys Leu  
290 295 300

45 Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
305 310

(2) INFORMATION FOR SEQ ID NO:12:

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
-55 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

60 AGCGGATAAC AATTCACAC AGG 23

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGTCTTTC CAGAGGGTAG T 21

10

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
15 (B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

20

Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu  
1 5 10 12

1038523796 3140204